



#4

N-TERMINAL AMINOACID SEQUENCES

Position	A	B	C
01			LEU
02			ALA
03			VAL
04			PRO
05		ALA	ALA
06		SER	SER
07		---	ARG
08	----**	---	ASN
09	GLN	GLN	GLN
10	SER	SER	SER
11	SER	SER	SER
12	---	---	GLY
13	ASP	ASP	ASP
14	THR	THR	THR
15	VAL	VAL	VAL
16	ASP	ASP	ASP
17	GLN	GLN	
18		GLY	
19		TYR	
20		GLN	
21		ARG	
22		PHE	
23		SER	
24		GLU	
25		THR	
26		SER	
27		HIS	
28		LEU	
29		ARG	
30		(GLY)*	
31		GLN	
32		TYR	
33		ALA	
34		PRO	
35		PHE	
36		PHE	
37		(ASP)	
38		LEU	
39		ALA	

FIG. 1A



PEPTIDE AMINOACID SEQUENCES

	A	B	C	D	E
Position					
01	GLN	(TRP)*	MET	ALA	VAL
02	-----**	SER	MET	SER	VAL
03	GLN	PHE	GLN	SER	ASP
04	ALA	ASP	CYS	ALA	----
05	GLU	THR	GLN	GLU	ARG
06	GLN	ILE	ALA	LYS	PHE
07	GLU	SER	GLU	GLY	PRO
08	PRO	THR	GLN	TYR	TYR
09	LEU	SER	GLU	ASP	THR
10	VAL	THR	PRO	LEU	GLY
11	(ARG)	VAL	LEU	VAL	----
12	VAL	ASP	VAL	VAL	ALA
13	LEU	THR	ARG		
14	VAL	LYS	VAL		
15	ASN	LEU	LEU		
16	(ASP)	SER	VAL		
17	(ARG)	PRO	ASN		
18	(VAL)	PHE	ASP		
19	VAL	(CYS)	ARG		
20	PRO	(ASP)			
21		LEU			
22		PHE			
23		THR			

FIG. 1B



N-TERMINUS 100KD PROTEIN

Position

01	VAL
02	VAL
03	ASP
04	GLU
05	ARG
06	PHE
07	PRO
08	TYR
09	THR
10	GLY

FIG.1C



10079709-1109992

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
Peptide C: Leu-Ala-Val-Pro-Ala-Ser-Arg-Asn-Gln-Ser-Ser-Gly-Asp-Thr-Val-Asp
Peptide B: Ala-Ser-*****Gln-Ser-Ser-****-Asp-Thr-Val Asp-Gln-Gly-Tyr-Gln-
Peptide A: *****Gln-Ser-Ser-****-Asp-Thr-Val-Asp-Gln

Possible
codons:5' CTG-GCG-GTG-CCG-GCG-TCG-CCG-AAT-CAA-TCG-TCG-GGG-GAT-ACG-GTG-GAT-CAA-GGG-TAT-CAA-
A A A A A A A A A A A A A A A A C G A C G
T T T T T T T T T T T T T T T
C C C C C C C C C C C C C C C
TTA AGT AGA AGT AGT AGT AGT AGT
G C G C C C C C C C C C C C C

AB1024: 3'-CGG-CAG-GGG-CCG-TCG-GCG-TTG-GTC-TCG-CCG-CTG-TGG-CAG-CTG-GTC
AB1065: 3'-CCG-CTG-TGG-CAC-CTG-GTC A
AB1066: A G
AB1067: A
AB1068: A
AB1069: A A A G A
AB1070: A A A G A
AB1226: 3'-CAG-CTG-GTC-CCG-ATG-GTC C A A
AB1227: 3'-CAG-CTG-GTC-CCG-ATG-GTC C A T A A T
AB1298: 3'-CTG-TGG-CAG-CTG-GTG-CCG-ATG-GTC A C C A T C A T

FIG.2A-1



1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
Peptide A: (Gln- ? -Gln-Ala-Glu-Gln-Glu-Pro-Leu-Val-(Ser/Arg)-Val-Leu-Val-(Asp/Asn)

CAG-??-CAG-GCG-GAG-CAG-GAG-CCG-CTG-GTG-(TCG/CGG)-GTG-CTG-GTG-(GAT/AAT)
A A A A A A A A A A A A A A C C
T T T T T T T T T T T T T T
C C C C C C C C C C C C C C
TTG AGT AGG TTG
A C A

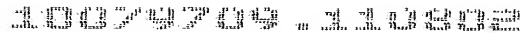
AB1295: 3'-GTC.CGC.CTC.GTC.CTC.GGG.GAG.CA-5'
T G T T T C A C

16 17 18 19 20 21 22
-Asp/Thr/Arg-(Arg/Val)-Val-Pro-(Pro)-Met-Gly

-GAT/ACG/CGG-(CGG/GTG)-GTG-CCG-(CCG)-ATG-GGG
C A A A A A A A A A
T T T T T T T T T T
C C C C C C C C C C
AGG AGG
A A

FIG.2B-1

10079709.110000



(TGG)-TCG-TTT-GAT-ACG-ATA-TCG-ACG-TCG-ACG-GTG-GAT-ACG-AAG-CTG-TCG-CCG-TTT-	A	C	C	A	T	A	A	A	A	A	A	A	A	C
	T			T	C	T	T	T	T	T	T	T	T	T
	C		C	C		C	C	C	C	C	C	C	C	C
	AGT					AGT		AGT		AGT		TTG	AGT	
	C					C		C		A		A	C	

AB1296 : 3'-AAG. CTG. TGC. TAG. AGG. TGG. AGG. TGG. CAC. CTG. TGC. TTC-5'
TCC C TCC C AB1297: 3'-GGC.AAG.
G

[illegible]

(ACG). (CTG). GAG. AAG. TGC. (TGC). (CTG). (CTC). (ACG). (TAG). (T)-5'

C G G G

FIG.2B-2



5'-TTT-TCG-TAT-GGG-GCG-GCG-ATA-CCG-CAG-TCG-ACG-CAG-GAG-AAG-CAG-TTT-TCG-CAG-GAG-TTT-CGG-GAT-GGG

AB1025: 3'-ATG-CCG-CCG-CGG-TAG-GGG-GTC-TCG-TGG-GTC-CTC-TTC-GTC-AAG-TCG-GTC-CTC-AAG-GC-5
AB1026: 3'-GTC-CTC-TTC-GTC-AAG-TCG-GTC-CTC-AAG-GC-5

AB1027: 3'-ATG-CCG-GCG-CGC-TAA-GGC-GTC-5'

FIG. 3



100/9709-110002

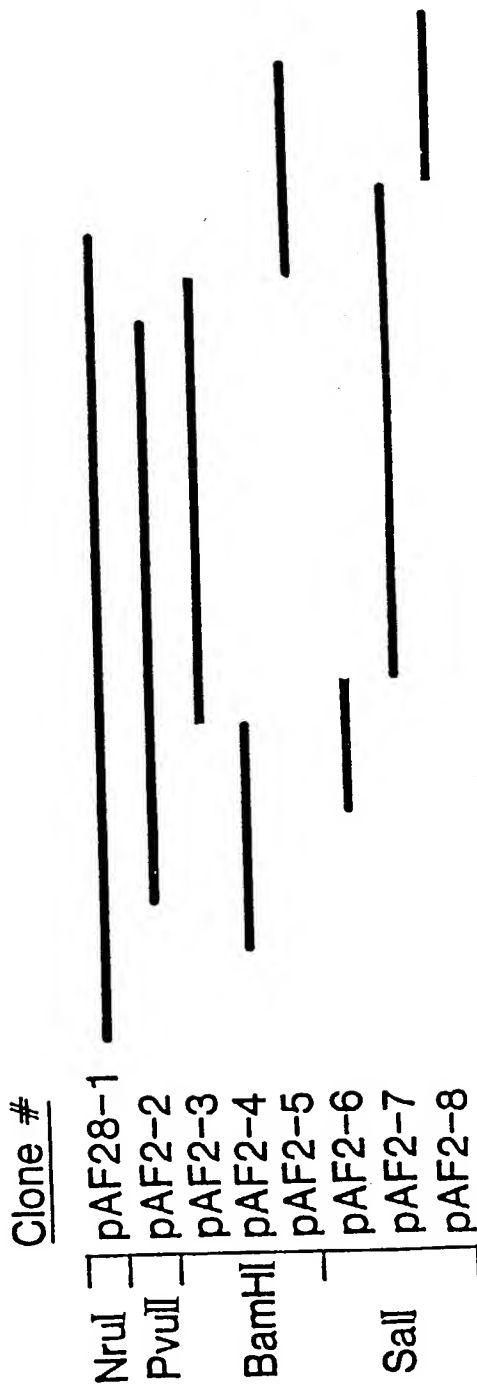
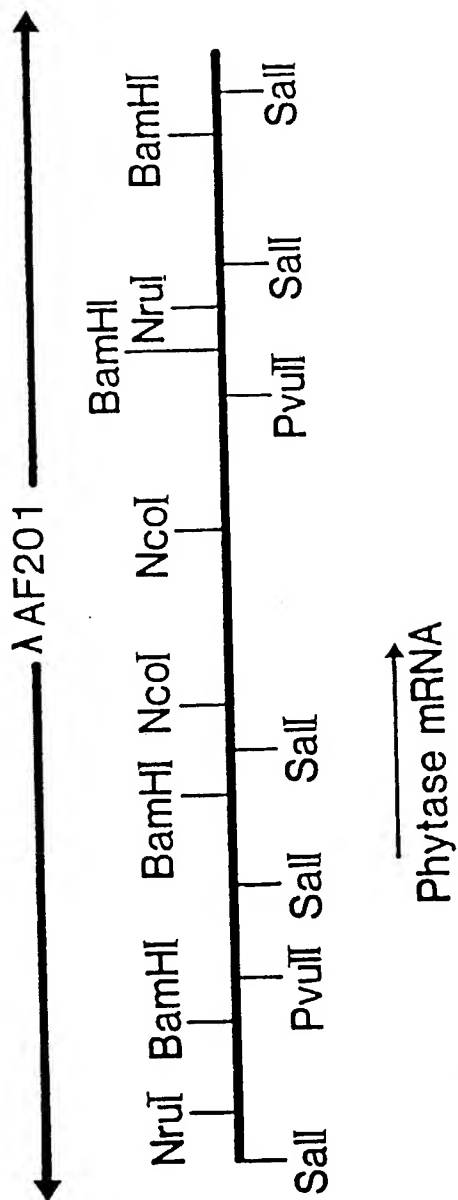


FIG.4

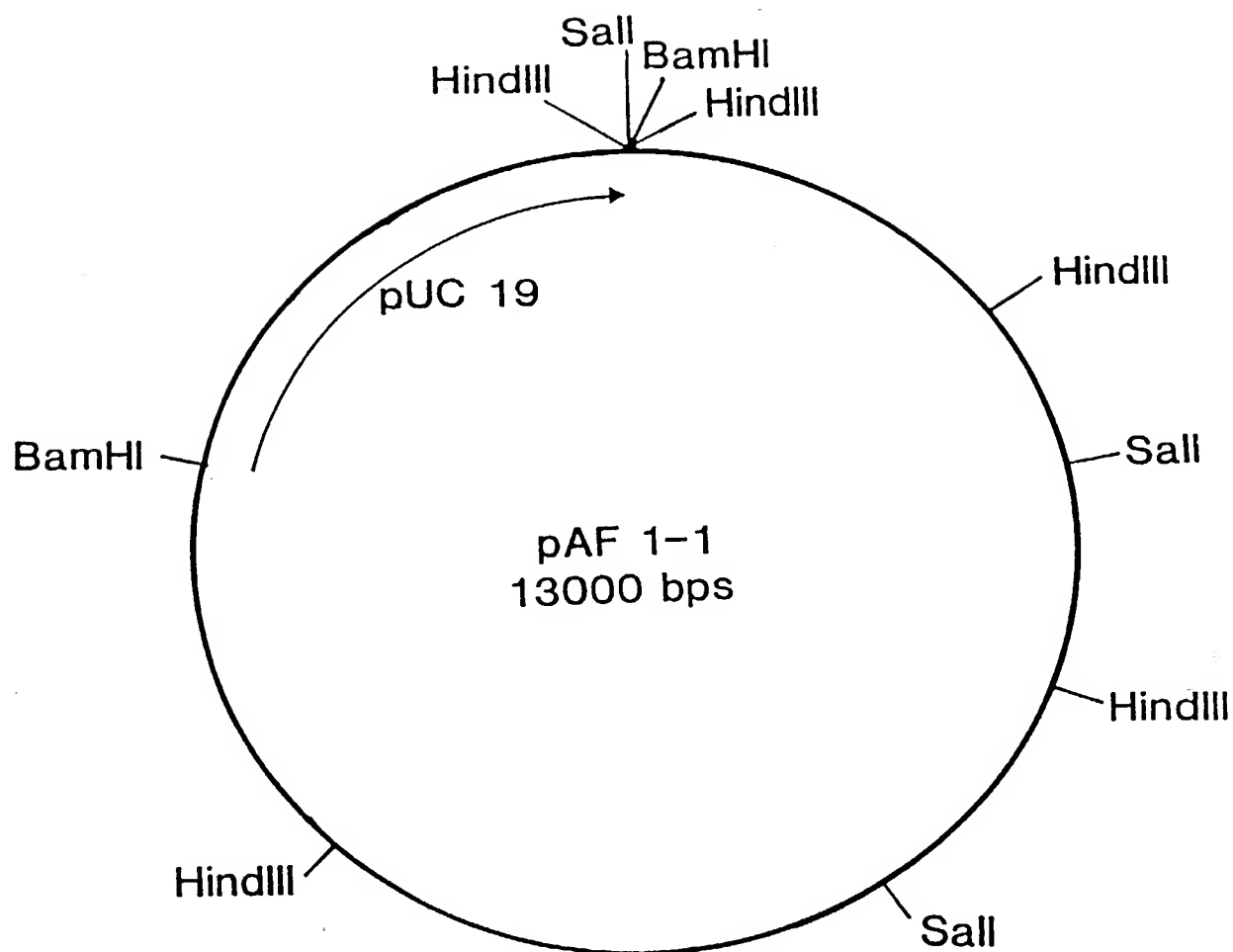


FIG.5



GTGGACTTCCCGTCCTATTCCGGCCTCGTCCGCTGAAGATCCATCCCACCA
 SalI
 TTGCACGTGGGCCACCTTTGTGAGCTTCTAACCTGAACTGGTAGAGTATC 100
 ACACACCATGCCAAGGTGGGATGAAGGGGTATATGAGACCGTCCGGTCC
 GGCGCGATGGCCGTAGCTGCCACTCGCTGCTGTGCAAGAAATTAATTCTC 200
 ATAGGCATCATGGGCGTCTCTGCTGTTCTACTTCCTTTGTATCTCCTGTC
 translation start
 TGGGTATGCTAAGCACCACAATCAAAGTCTAATAAGGACCCTCCCTTCCG 300
 start<-----
AGGGCCCCTGAAGCTCGGACTGTGTGGGACTACTGATCGCTGACTATCTG
 --intron-----
 TGCAGAGTCACCTCCGGAAGTGGCAGTCCCCGCCTCGAGAAATCAATCCAG 400
 ->end
 TTGCGATACGGTCGATCAGGGGTATCAATGCTTCTCCGAGACTTCGCATC
 TTTGGGGTCAATACGCACCGTTCTTCTCTCTGGCAAACGAATCGGTCATC 500
 TCCCCTGAGGTGCCCGCCGGATGCAGAGTCACTTTCGCTCAGGTCCTCTC
 CCGTCATGGAGCGCGGTATCCGACCGACTCCAAGGGCAAGAAATACTCCG 600
 CTCTCATTTAGGAGATCCAGCAGAACGCGACCACTTTGACGGAAAATAT
 GCCTTCCTGAAGACATACAACCTACAGCTTGGGTGCAGATGACCTGACTCC 700
 CTTCCGAGAAACAGGAGCTAGTCAACTCCGGCATCAAGTTCTACCAGCGGT
 ACGAATCGCTCACAAGGAACATCGTTCCATTCATCCGATCCTCTGGCTCC 800
 AGCCGCGTGATCGCCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGCAC
 CAAGCTGAAGGATCCCTCGTGCCAGCCCGGCCAATCGTCGCCCAAGATCG 900
 BamHI
 ACGTGGTCATTTCCGAGGCCAGCTCATCCAACAACACTCTCGACCCAGGC
 ACCTGCACTGTCTTCGAAGACAGCGAATTGGCCGATACCGTCGAAGCCAA 1000

FIG.6A



TTTCACCGCCACGTTTCGTCCCTCCATTCGTCAACGTCTGGAGAACGACC
 TGTCCGGTGTGACTCTCACAGACACAGAAGTGACCTACCTCATGGACATG 1100
 TGCTCCTTCGACACCATCTCCACCAGCACCGTTCGACACCAAGCTGTCCCC
 CTCTGTGACCTGTTACCCATGACGAATGGATCAACTACGACTACCTCC 1200
 AGTCCTTGAAAAAGTATTACGGCCATGGTGCAGGTAACCCGCTCGGCCCG
 ACCCAGGGCGTCGGCTACGCTAACGAGCTCATCGCCCGTCTGACCCACTC 1300
 GCCTGTCCACGATGACACCAGTTCCAACCACACTTTGGACTCGAGCCCGG
 CTACCTTTCCGCTCAACTCTACTCTCTACGCGGACTTTTCGCATGACAAC 1400
 GGCATCATCTCCATTCTCTTTGCTTTAGGTCTGTACAACGGCACTAAGCC
 GCTATCTACCACGACCGTGGAGAATATCACCCAGACAGATGGATTCTCGT 1500
 CTGCTTGGAACGGTTCCGTTTGCTTCGCGTTTGTACGTCGAGATGATGCAG
 TGTCAGGCGGAGCAGGAGCCGCTGGTCCGTGTCTTGGTTAATGATCGCGT 1600
 TGTCCCGCTGCATGGGTGTCCGTTGATGCTTTGGGGAGATGTACCCGGG
 ATAGCTTTGTGAGGGGGTTGAGCTTTGCTAGATCTGGGGGTGATTGGGCG 1700
 GAGTGTTTTGCTTAGCTGAATTACCTTGATGAATGGTATGTATCACATTG
 translation stop
 CATATCATTAGCACTTCAGGTATGTATTATCGAAGATGTATATCGAAAGG 1800
 ATCAATGGTGACTGTCACTGGTTATCTGAATATCCCTCTATACCTCGTCC
 CACAACCAATCATCACCTTTAAACAATCACACTCAACGCACAGCGTACA 1900
 AACGAACAAACGCACAAAGAATATTTTACACTCCTCCCCAACGCAATACC
 AACCGCAATTCATCATACCTCATATAAATACAATACAATACAATACATCC 2000

FIG.6B



310397139-1103032

ATCCCTACCCTCAAGTCCACCCATCCTATAATCAATCCCTACTTACTTAC
TTCTCCCCCTCCCCCTCACCTTCCCAGAACTCACCCCCGAAGTAGTAAT 2100
AGTAGTAGTAGAAGAAGCAGACGACCTCTCCACCAATCTCTTCGGCCTCT
TATCCCCATACGCTACACAAAACCCCCACCCGTTAGCATGCACTCAGAA 2200
AATAATCAAAAATAACTAAGAAGGAAAAAAGAAGAAGAAAGGTTACAT
ACTCCTCTCATACAACTCCAAGACGTATACATCAAGATGGGCAATCCCA 2300
CCATTACTGATATCCATCTATGAACCCATTCCCATCCCACGTTAGTTGAT
TACTTTACTTAGAAGAAGAAAAGGGAAGGGAAGGGAAGGAAGTGGATGG 2400
GATTGAGTTAGTGCTCACCGTCTCGCAGCAAGTTTATATTCTTTTGTTG
GCGGATATCTTCACTGCTCCTGCTGGACGTTGTCACGGGGTGGTAGTGG 2500
TTGGCGGTGGTGAGGGTCCATGATCACTCTTGGTTTGGGGGGTGTGTT
GTCGTTGTTGTTGTTGTTGGGTGGGCATTTTCTTTTCTTCACTTGGGGAT 2600
TATTATTTGGAATTGGTTAGTTTGAGTGAGTGGGTAATATTGAATGGGTG
ATTATTGGGAATGAAGTAGATTGGCTATGAATGGTTGATGGGATGGAAT 2700
GAATGGATGGATGAATAGATGGAGGCGGAAAAGTCAGGTGGTTTGAGGTT
CGGATTATTATCTTTGTGCCTGAGGCATCACTCTCCATCTATGTTGTTCT 2800
TTCTATACCGATCTACCAGAGCTAAGTTGACTGATTCTACCACAGTGCAC
AATAAGTATGTACTTATTTTATTTAGAGTATTTAGATTAACCCGCTGTGC 2900
TATTTGCCGTAGCTTTCCACCCAATTCGAAGTTCGAAGAATTAAAACTC
ATCCTACAGTACAGAATAGAAGTAAAAGGAGAAGAGAAAAACAAGATAAT 3000

FIG.6C



10079709, 1109999

ACAACCAGTCCAGGTCCATTCTAGATCTCGAATGACCACCAAATAAGAAA
GCAACAAGCAAGTAAGCAAAGCATAAGTCTAAATGAACGCCAATAACTTC 3100
ATCGCCTGCCTTTGAAACTGAACGCTATGCACGAATGGCTCGAAATGATT
CCCTTAACTCCGTAGTATTGAGAGTGAGAGGAAAAGAAAAAAGAGACAG 3200
AAAAGCTGACCATGGGAAAGAAGCATGATCAGTCGGGAATGGATCTGCGG
GTTGAGATAGATATGAGTTGCCTCGCAGATCCGGTGACAAGATAAGAGAA 3300
TTGGGAGATGTGATCAGCCACTGTAACCTCATCAAGCATCGACATTCAAC
GGTCGGGTCTGCGGGTTGAGATGCAAGTTGAGATGCCACGCAGACCCGAA 3400
CAGAGTGAGAGATGTGAGACTTTTGAACCCTGTGACTTCATCAAGCATC
AAAACACACTCCATGGTCAATCGGTAGGGTGTGAGGGTTGATATGCCAG 3500
GTTGATGCCACGCAGACCCGAACCGACTGAGAAATATGAAAAGTTGGAC
AGCCACTTCATCTTCATCAAGCGTAAACCCCAATCAATGGTAAATCGAA 3600
AACGAATCTGCGGGCTGATGTGGAAATGAGACGAATGCCTCGCAGATTCTG
AAGACACGTAAATCGAGATGAACAATCACTTTAACTTCATCAAAGCCTTA 3700
AATCACCCAATGGCCAGTCTATTCTGGGTCTGCGGGTTGAGGTTCTGTG
AGATGCCACGCAGACTGCGAACATGCGATGCATTATAAGTTGGACGAGTG 3800
TAGACTGACCATTGATAACCGAGATAAACAAATCACTTCAACTTCATCAA
GCCTTAAATCACTCAATGGCCAGTCTGTTTTCGGGTCTGCGGGCTGATACC 3900
CAAGTTGCGATGCCACGCAGACTGCAAACATTGATCGAGAGACGAGAAAA
ACAACGCACTTTAACTTCAACAAAAGCCTTTCAATCAGTCAATGGCCAGT 4000

FIG.6D



10079709.1.10302

CTGTTGCGGGTCTGCGGGCTGATATGCGAGTTGAGGTGCCTCGCAGACCG
CGAACATGCGATGTAATTTCTTAGTTAGACGAGTGCCTGGCCATTGAGAA 4100
ACGAGAGAAACAACCACTTTAACTTCATGAAAGCCTTGAACCTACTCAATG
ACCCGTCTGTTGGCGGTCTGCGGGCTGATATTCGAGTTGAGATGCCACGC 4200
AGACCGCCAACATGCGATGTATCATGTAAGTTAGATGAGTGAAGTGGCCAT
TGAGAAACGAGAGAAACAACCACTTCATGAGAGCCTTAAATTATTCAA 4300
TGACCAGTCTGTTACGGTCTGCGGGTTGGTATGCGAGTGCAGGTGCCTC
GCAGACCGCGAACATGCGATGTTTTGATGGACGAGTGAAGCCTGACGAT 4400
CGAGAACTATCTCAGTTGGGTTGGCCATTTCGGCTGGCCGTTGGGTTTAGT
ATTAGGATCGTCAGGTTTGTCCGATGGAACGTTCCGTTTGCGTGCCTTGG 4500
CGCGACGAGCCCTCTCCTCGGGCTGATTCTGAAATTCTGCAATCAGGGCA
GCCGACGACCGGCGACGGGACGTCCTCCAGGAGCTGTGTTGAAGTTTCGG 4600
GGTGGCGGTCCAGAAGGGGGAGTTACATTAAAAGCCTCATAGATGTCTTT
GGGTGGTTCCGGGGGGCCCATCGCAAGATCTTCTGGAGTTGTGCGTCTGA 4700
TCATCTCTTGAGTGTAATTGCGACGCAGACCGAGCTTCAGGATTTTGGA
GGGCTGGATCGCTCCTGCTGACTCTTCCCTCAGCGGGCTTCGTCTCGGC 4800
AGTCTTCATTTCCGGCGGGCTGATCTTCCATCTCAGAATGGGATCGCTTTC
TGGTCGCTGCACCCGCTCCTCCCTTCAAGGTCAGCTTGATGCGCAGCGTC 4900
TTGGGCGGCTCAGCTGGTGGAGTTGGTTCCGGCTCTGGCTCCCTCCGGCG
TCGCTTGGGCACTTGAGTAGTCTCTGAGGCTTCGCCGCGGCGCGCTTTGC 5000



10079709 110303

GAGTCGGCTCCTTGGTCTCTTTGGCCTCTTTCACTTCACCTGGACCGTCT
TTCGGGGCGGTTTCATCGTGCTGAGCGATCAAGGTTTGGATGTAGGCAGC 5100
CGGCATCATTCGATCAACGGCAATTCCTCTCTTGCGGGCCTCCTCCCGAG
CCTTGATTGTTCGCCTTGACCTCGTCCACGTTTTCGAAGAAGAAAGGCATC 5200
TTGTTATCCTGAGGCAAGTTGCGCTCTCCCATGCGTGCGGATATCCGAAG
ATGCGGTCCTTCTCGAACTGTTTCATGAGACTTCAGACGAATTGGAGGCTG 5300
GGGGAGCAATTTGTCTCCGTAGGTGTTGTTAGGGCGGAACCAAGAATAGC
CTTCGCCTACAACGACAAGCTCTTCGCCAAATTTATTTTTTTGGCCTGTÀ 5400
AAAACGAACCCATCCTCGTCACTCCACCGGTGCGTCTCGGACGTAGAGAT
TGGCTTACTTATTCCCTCAACGCCGATCTCTGCCTGGGGCTGCGCTTCGG 5500
ATGCGGCCTCGGTACGGCTCCGCCTCGGACTGCACCGCTGGAGTTTCGG
TCTTCTTCTCCTGCTTCTCCAGGTACTCCTTGCGTAACTCTTCGATCAGC 5600
CTCGGCTTCCGATGACTGCTCAAATTCTGGAGCAACAGCTGCCGCGGCCA
GGTCAAGCAGGCGGTTTGCTAAACTGCCCATTTTCCATCGACACCTGCC 5700
TCCGACGCCTGTGCAAAACCAGCTGTTTTCGCATGGCCTGTTTGTGGC
ACGCGTCTTCTTGACTGCTGCCTTGCCCTTTACTTCCTTGAGAGCAGACT 5800
CTGGCTTAGATGATGGTGCACGGTTTCTGCGGAAGCGCCGCTCAGATTCC
AAAGATTCCATAGCTTTAATGGTAGGCTTTCTGGTTCTTCCAGAAGTGCG 5900
CGCAGCTGACGTAGTGGTTGAGTAGCTGGCAGTTGGGGATCCTGGGCCCT
CATTGGAACCATCAAGACCAATTTGTTTCCATACATATCAGCATGGTAT 6000

FIG.6F



TCAAAAGGAAACTTTCGCCGTACGGAGTACTGCGTTCGATTCCGGGTGT
 ATCCAAGTCGTATCCAGACATGGTGTGCAATTCAGCCTTGCTGTCAAGAG 6100
 CAGGGGTACTTTCAATGCTGTGTCAGCAACCACGCGGCCAAAGGGCGTCTTC
 GGGAAAGAAGGTGTTTCAAGAGAAGCGTCAATCCACGGCCTGGCTTGCGGC 6200
 GTTGATTGCAGACTTTCGAGTAGATCGCTGAGGTCGCGAACTGGTTCGAG
 TAGCAACCTGTGAATTGGCAGCCTTGTGACTGCTTCGATTCACTGCAGAG 6300
 ACGGAGTAGACTGCACTGATTTGGAATTCTGAGTCGCAGCCATTCTGGAT
 TTGCGTTCGGCGCGACGAGATCTCGCAGTCGTGGTACGAGGAGTAGAGCG 6400
 AGGCTGCGTAGCAGTGTTGCAAGCTTGGTGCTAGCCTCCTGGGCTTCAGC
 AGCTTCAGCAGTGGTGGCAGACGCAGCAGAATTAGCGGAGCTTTATCGGC 6500
 TTTGCCGCTCTGAGCGTTGGGAGTAGAAGTGAGAGAAGAGGTAGAGTCCA
 CGGAAGAAGTCTTCTCGCTGTTCTCAAAGCCGTTTCAGCTTTGCTGGCATA 6600
 GACTTACGCGTCTTGCGGCTGTTGGAAGCGGAAGAGTTCATGGCGGGAGA
 GGAGACGTTAGAAGTAGACATGGTGGGGTTTGTTGACGGGTTTTGAGTAA 6700
 CAAGAGACTTGCGTCGATCTTTGAGTGTTCTTGACAGAAAGTTATGCAAC

GTCGAC 6756
 SalI

FIG.6G



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PHYTASE LOCUS

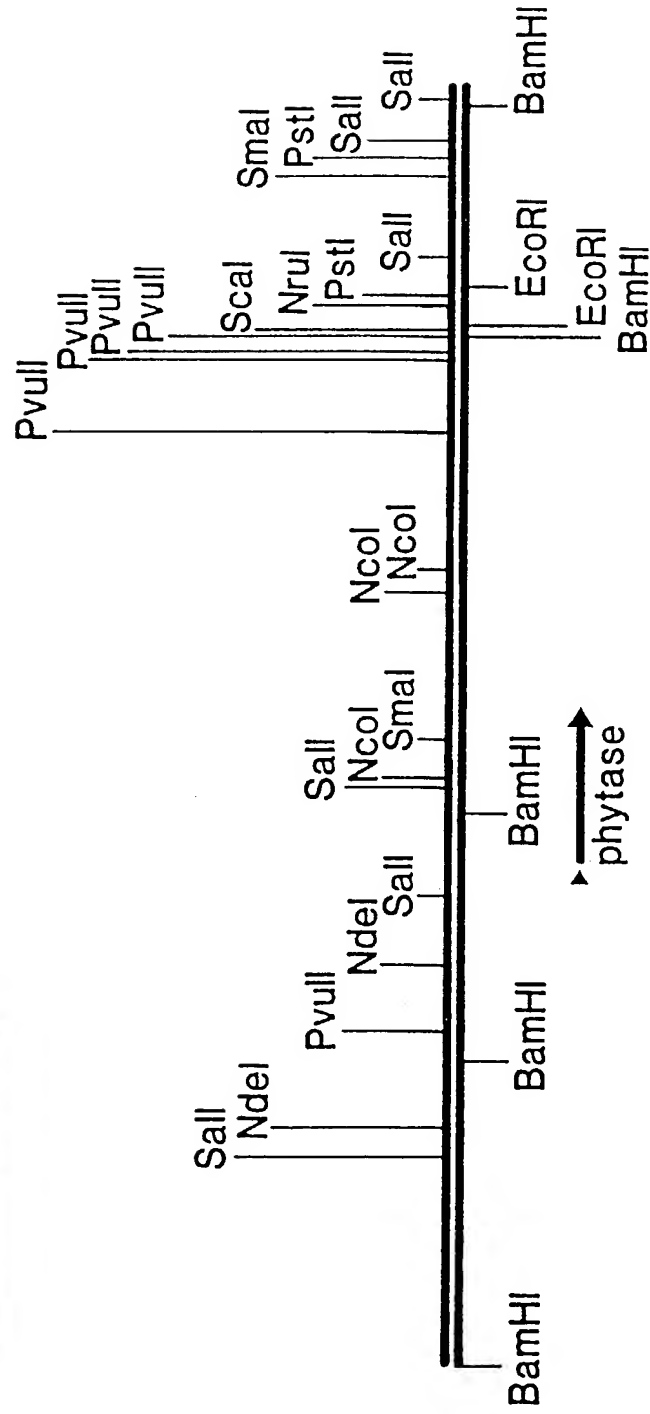


FIG.7



10079709.110302

ATGGGCGTCTCTGCTGTTCTACTTCCTTTGTATCTCCTGTCTGGAGTCAC
M G V S A V L L P L Y L L S G V T
-23 -20 -10

CTCCGGACTGGCAGTCCCCGCCTCGAGAAATCAATCCAGTTGCGATACGG 100
S G L A V P A S R N Q S S C D T
, -1 +1 , 10

TCGATCAGGGGTATCAATGCTTCTCCGAGACTTCGCATCTTTGGGGTCAA
V D Q G Y Q C F S E T S H L W G Q
20

TACGCACCGTTCTTCTCTCTGCGCAAACGAATCGGTCATCTCCCCTGAGGT 200
Y A P F F S L A N E S V I S P E V
30 40

GCCCGCCGGATGCAGAGTCACTTTCGCTCAGGTCCTCTCCCGTCATGGAG
P A G C R V T F A Q V L S R H G
, 50 , 60

CGCGGTATCCGACCGACTCCAAGGGCAAGAAATACTCCGCTCTCATTGAG 300
A R Y P T D S K G K K Y S A L I E
, 70 ,

GAGATCCAGCAGAACGCGACCACCTTTGACGGAAAATATGCCTTCCTGAA
E I Q Q N A T T F D G K Y A F L K
80 , 90

GACATACAACACTACAGCTTGGGTGCAGATGACCTGACTCCCTTCGGAGAAC 400
T Y N Y S L G A D D L T P F G E
, 100 , 110

AGGAGCTAGTCAACTCCGGCATCAAGTTCTACCAGCGGTACGAATCGCTC
Q E L V N S G I K F Y Q R Y E S L
, 120 ,

ACAAGGAACATCGTTCCATTTCATCCGATCCTCTGGCTCCAGCCGCGTGAT 500
T R N I V P F I R S S G S S R V I
130 , 140

CGCCTCCGGCAAGAAATTCATCGAGGGCTTCCAGAGCACCAAGCTGAAGG
A S G K K F I E G F Q S T K L K
, 150 , 160

ATCCTCGTGCCCAGCCCCGCCAATCGTCGCCCAAGATCGACGTGGTCATT 600
D P R A Q P G Q S S P K I D V V I
, 170 ,

TCCGAGGCCAGCTCATCAACAACACTCTCGACCCAGGCACCTGCACTGT
S E A S S S N N T L D P G T C T V
180 , 190

CTTCGAAGACAGCGAATTGGCCGATACCGTCGAAGCCAATTCACCGCCA 700
F E D S E L A D T V E A N F T A
, 200 , 210

FIG.8A



11009909.110902

CGTTCGTCCCCTCCATTCGTCAACGTCTGGAGAACGACCTGTCCGGTGTG
T F V P S I R Q R L E N D L S G V
220

ACTCTCACAGACACAGAAGTGACCTACCTCATGGACATGTGCTCCTTCGA 800
T L T D T E V T Y L M D M C S F D
230 240

CACCATCTCCACCAGCACCGTCGACACCAAGCTGTCCCCCTTCTGTGACC
T I S T S T V D T K L S P F C D
250 260

TGTTACCCCATGACGAATGGATCAACTACGACTACCTCCAGTCCTTGAAA 900
L F T H D E W I N Y D Y L Q S L K
270

AAGTATTACGGCCATGGTGCAGGTAACCCGCTCGGCCCCGACCCAGGGCGT
K Y Y G H G A G N P L G P T Q G V
280 290

CGGCTACGCTAACGAGCTCATCGCCCGTCTGACCCACTCGCCTGTCCACG 1000
G Y A N E L I A R L T H S P V H
300 310

ATGACACCAGTTCCAACCACACTTTGGACTCGAGCCCGGCTACCTTTCCG
D D T S S N H T L D S S P A T F P
320

CTCAACTCTACTCTCTACGCGGACTTTTCGCATGACAACGGCATCATCTC 1100
L N S T L Y A D F S H D N G I I S
330 340

CATTCTCTTTGCTTTAGGTCTGTACAACGGCACTAAGCCGCTATCTACCA
I L F A L G L Y N G T K P L S T
350 360

CGACCGTGGAGAATATCACCCAGACAGATGGATTCTCGTCTGCTTGGACG 1200
T T V E N I T Q T D G F S S A W T
370

GTTCCGTTTGCTTCGCGTTTGTACGTCGAGATGATGCAGTGTGAGGCGGA
V P F A S R L Y V E M M Q C Q A E
380 390

GCAGGAGCCGCTGGTCCGTGTCTTGGTTAATGATCGCGTTGTCCCGCTGC 1300
Q E P L V R V L V N D R V V P L
400 410

ATGGGTGTCCGGTTGATGCTTTGGGGAGATGTACCCGGGATAGCTTTGTG
H G C P V D A L G R C T R D S F V
420

AGGGGGTTGAGCTTTGCTAGATCTGGGGGTGATTGGGCGGAGTGTGTTTGC 1400
R G L S F A R S G G D W A E C F A
430 440

TTAG 1404

FIG.8B



10079709.110302

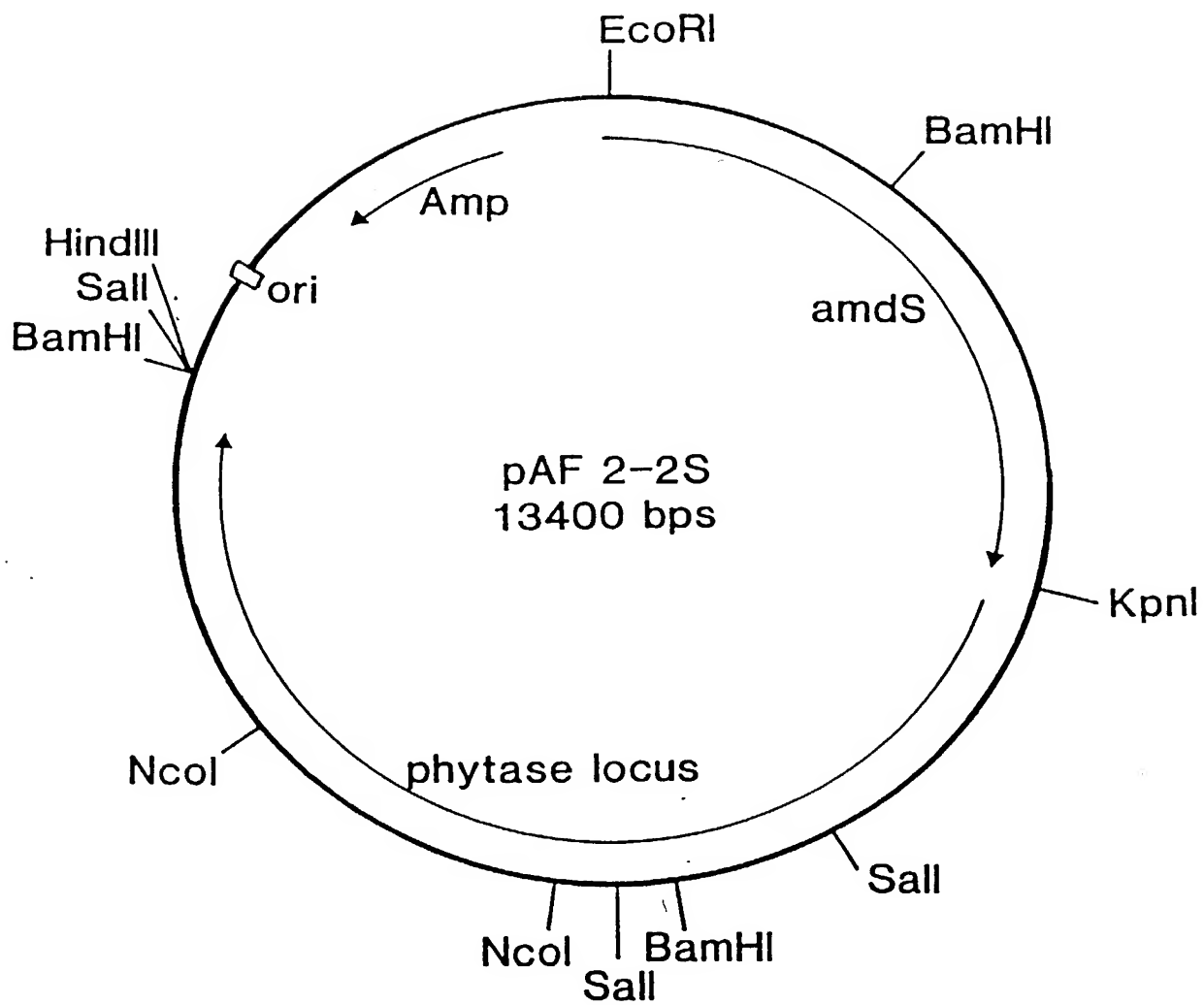


FIG.9



10079709 110802

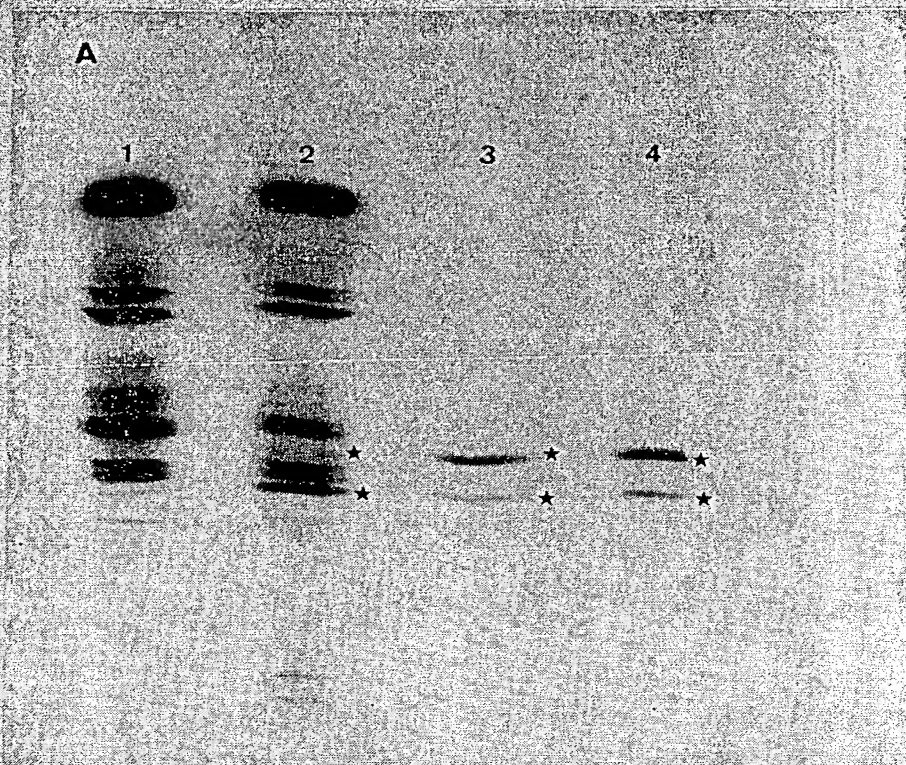


Figure 10A

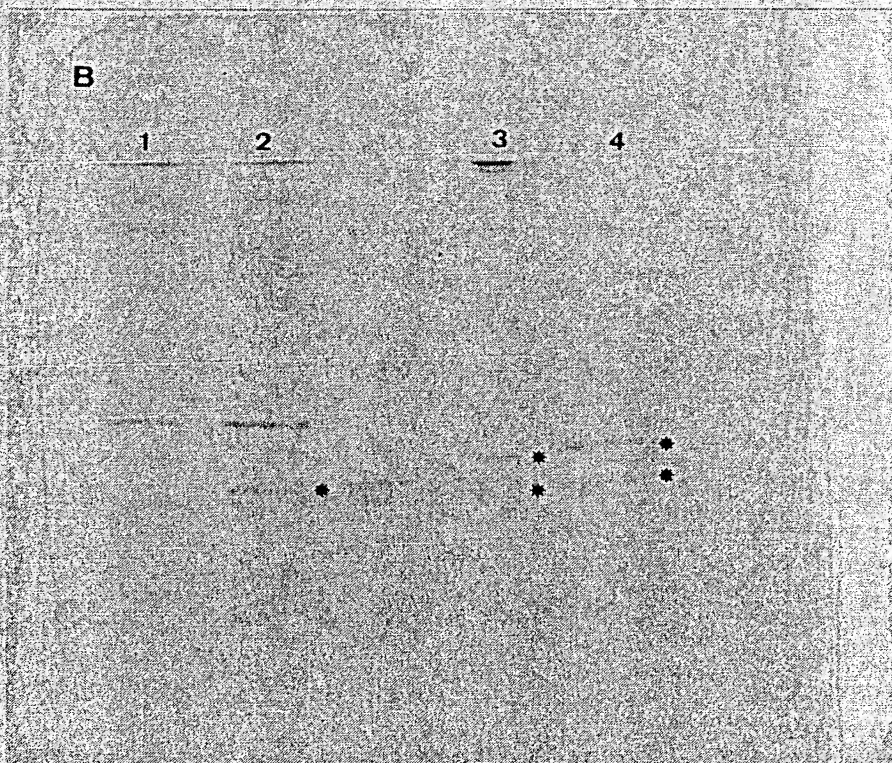


Figure 10B



10079709 .110802

A

1

2

3

4



Figure 11A

B

1

2

3

4

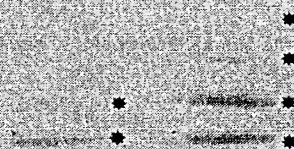


Figure 11B



10079709.110202

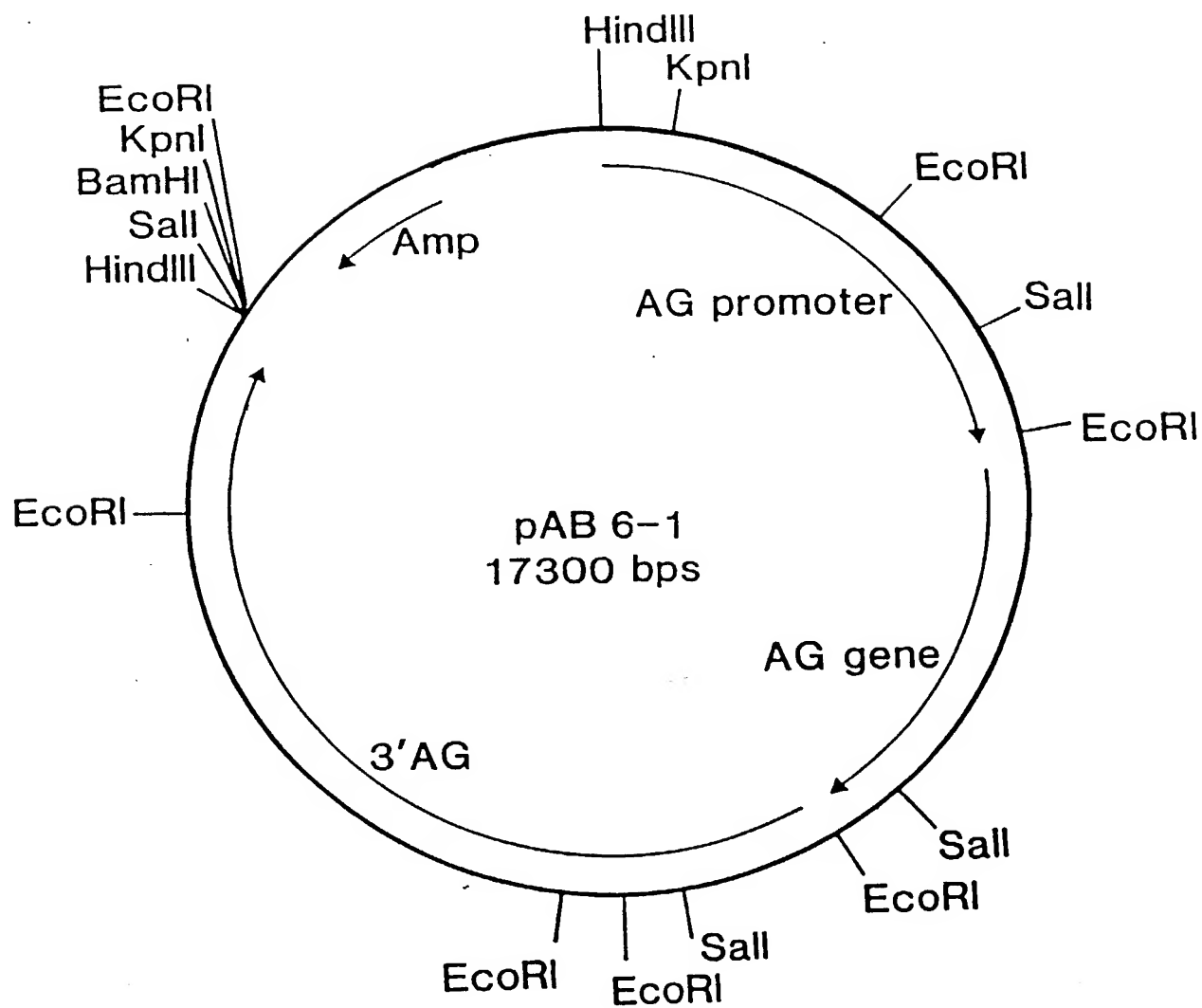


FIG. 12



10079709.110302

AG/PHYTASE GENE FUSIONS BY PCR

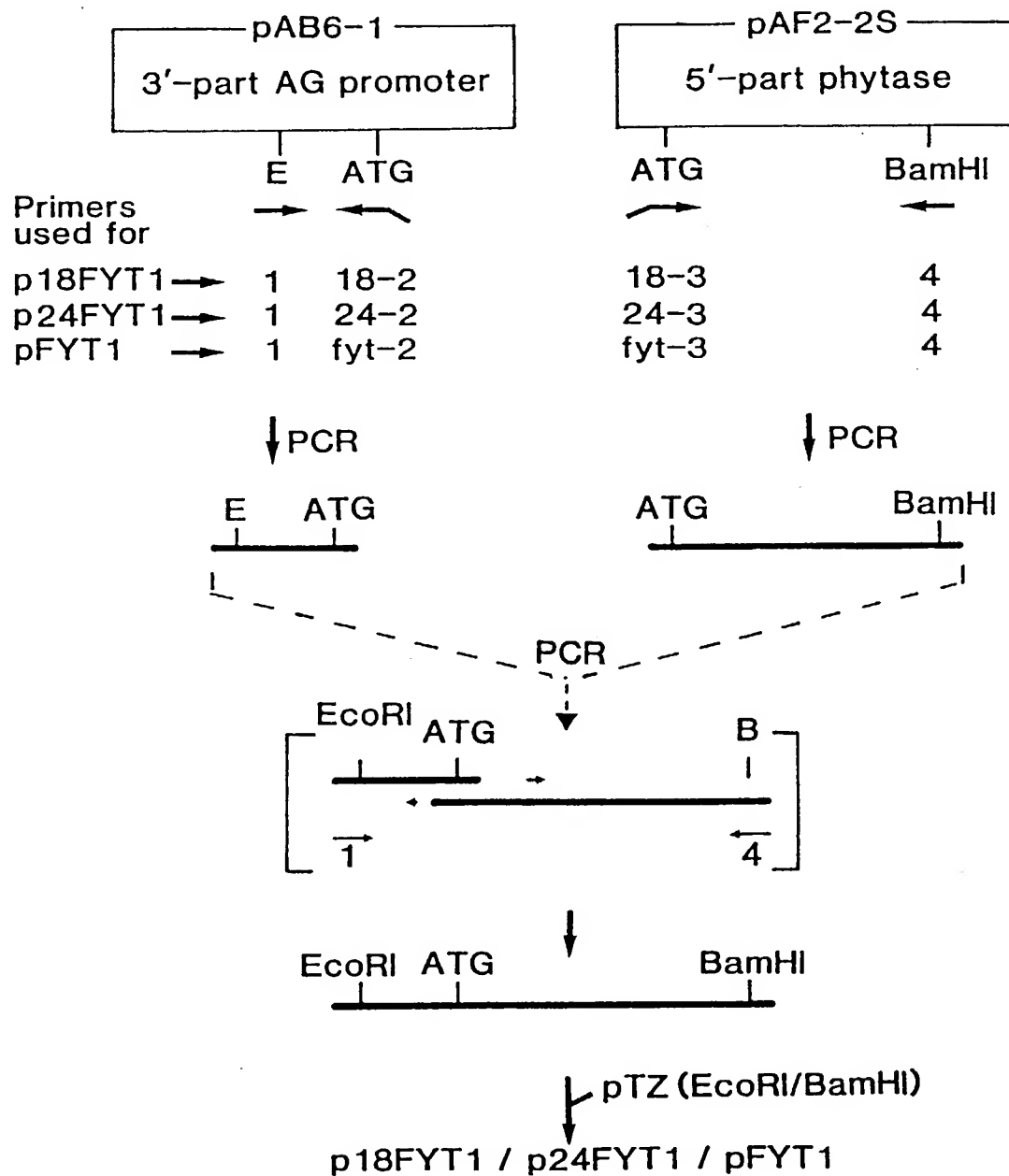


FIG. 13



11/11/2002 11:11:11

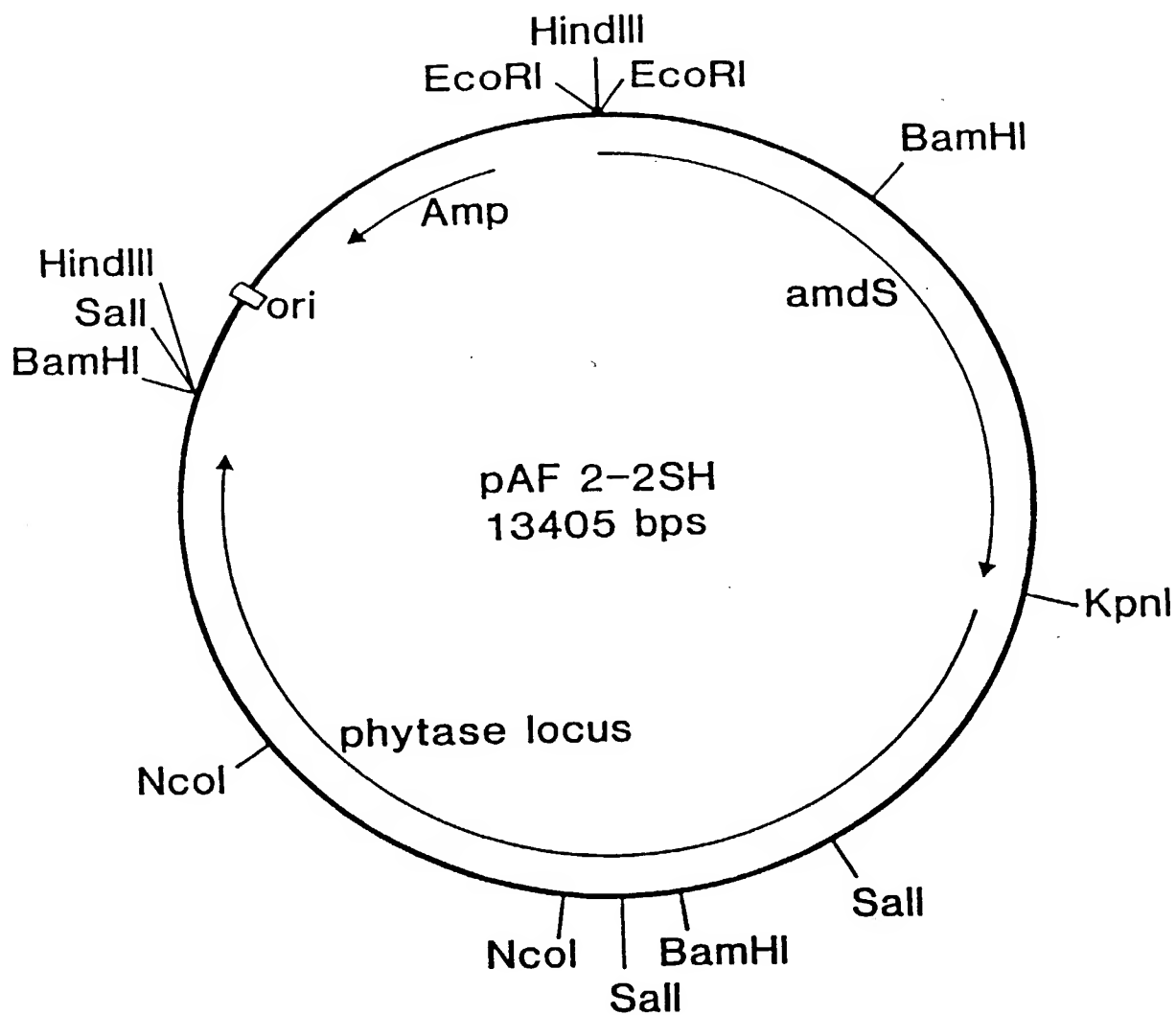


FIG. 14

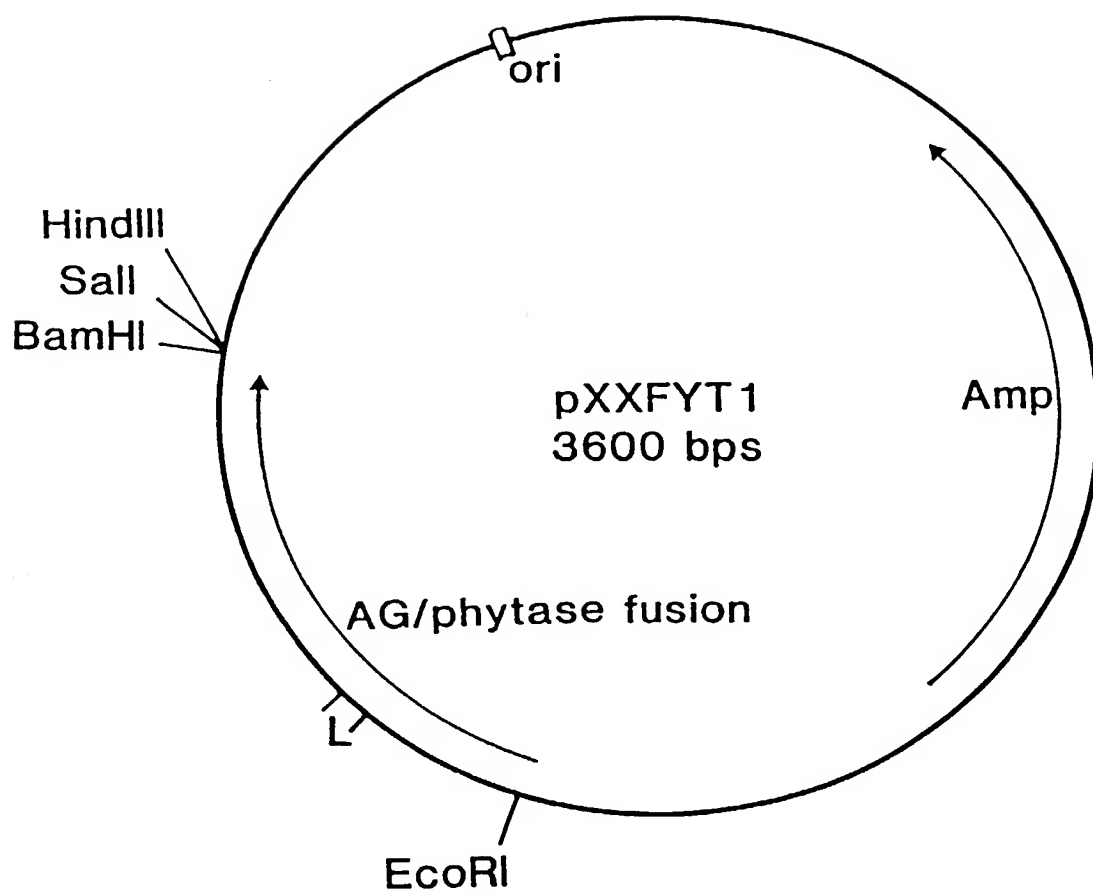


FIG. 15A



110329293 110329293

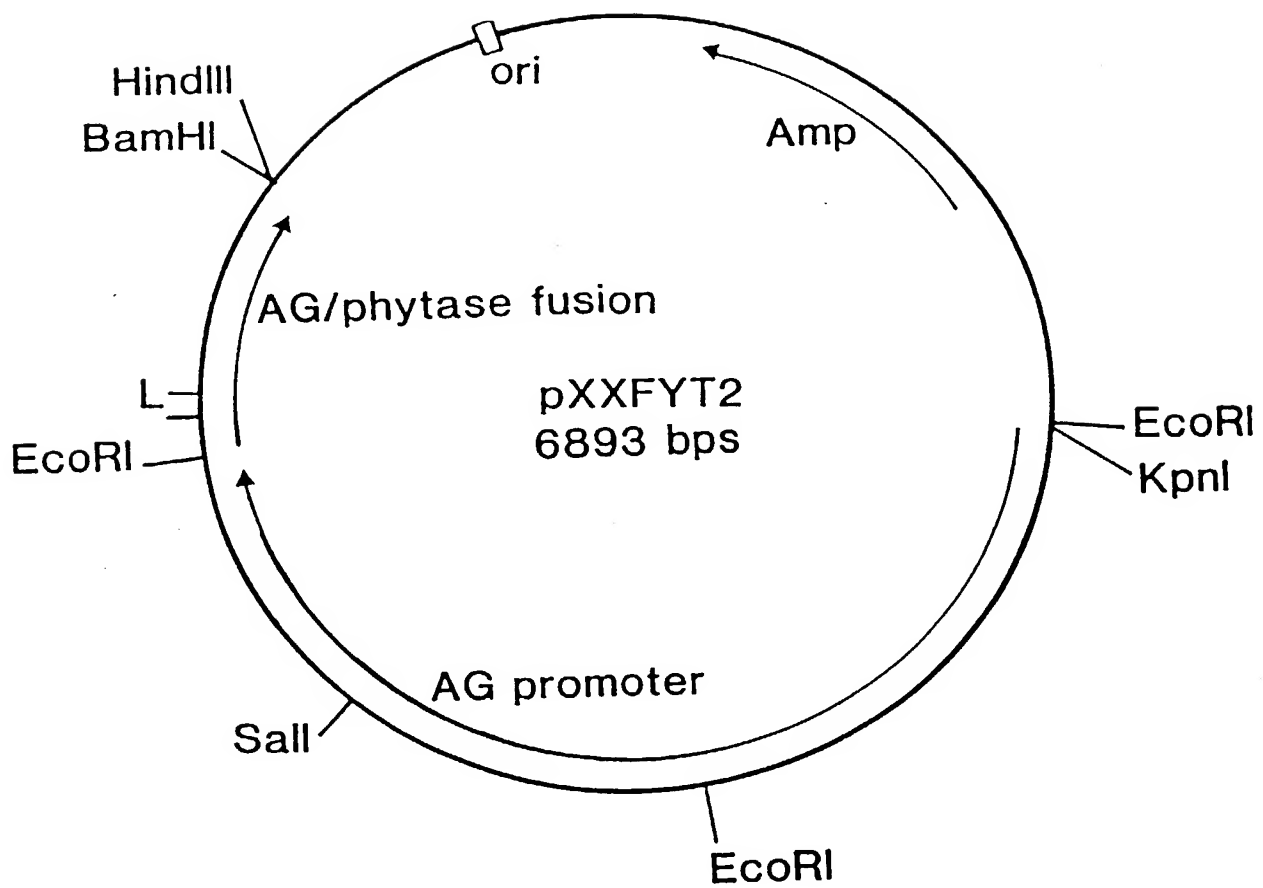


FIG. 15B

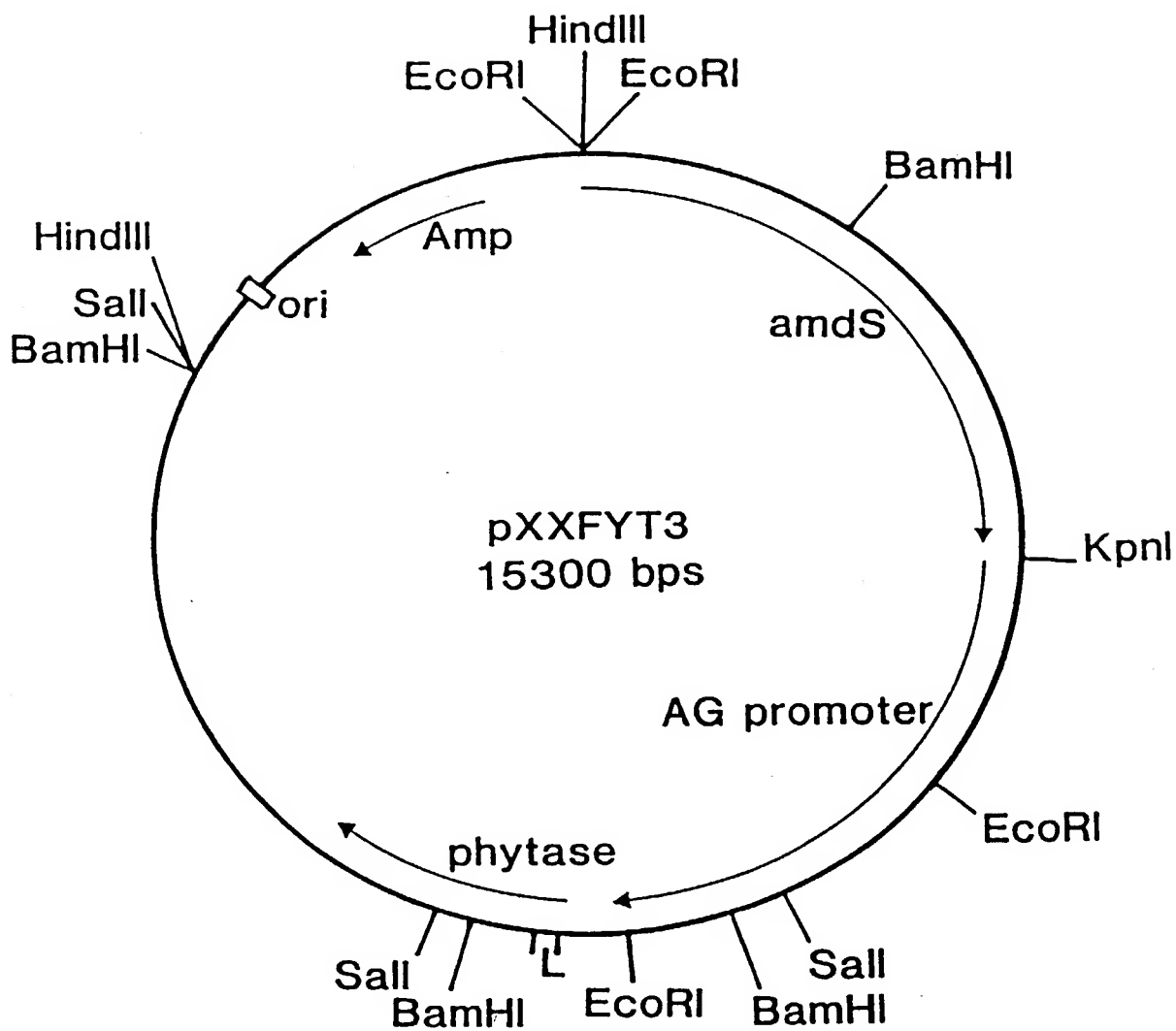


FIG. 15C

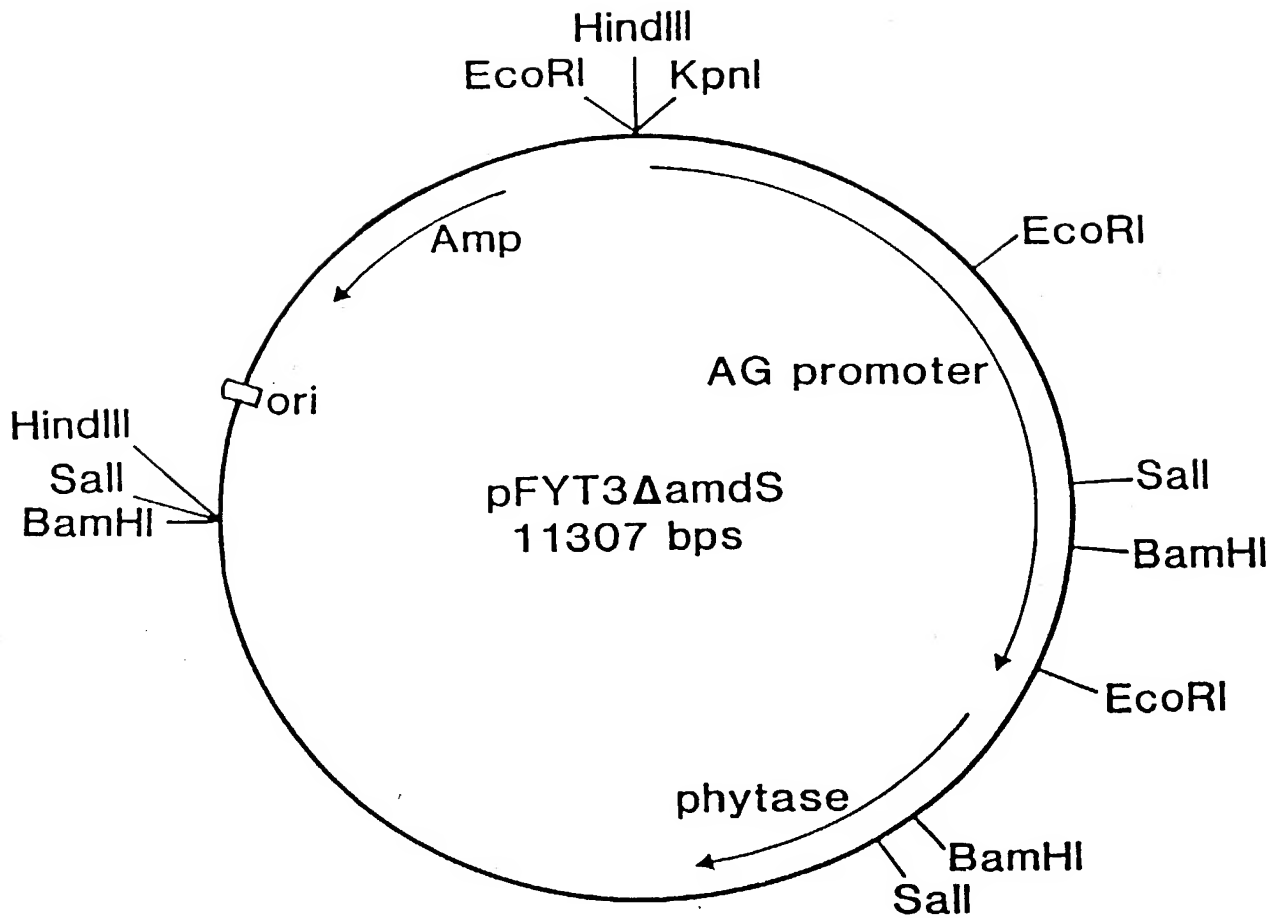


FIG. 16

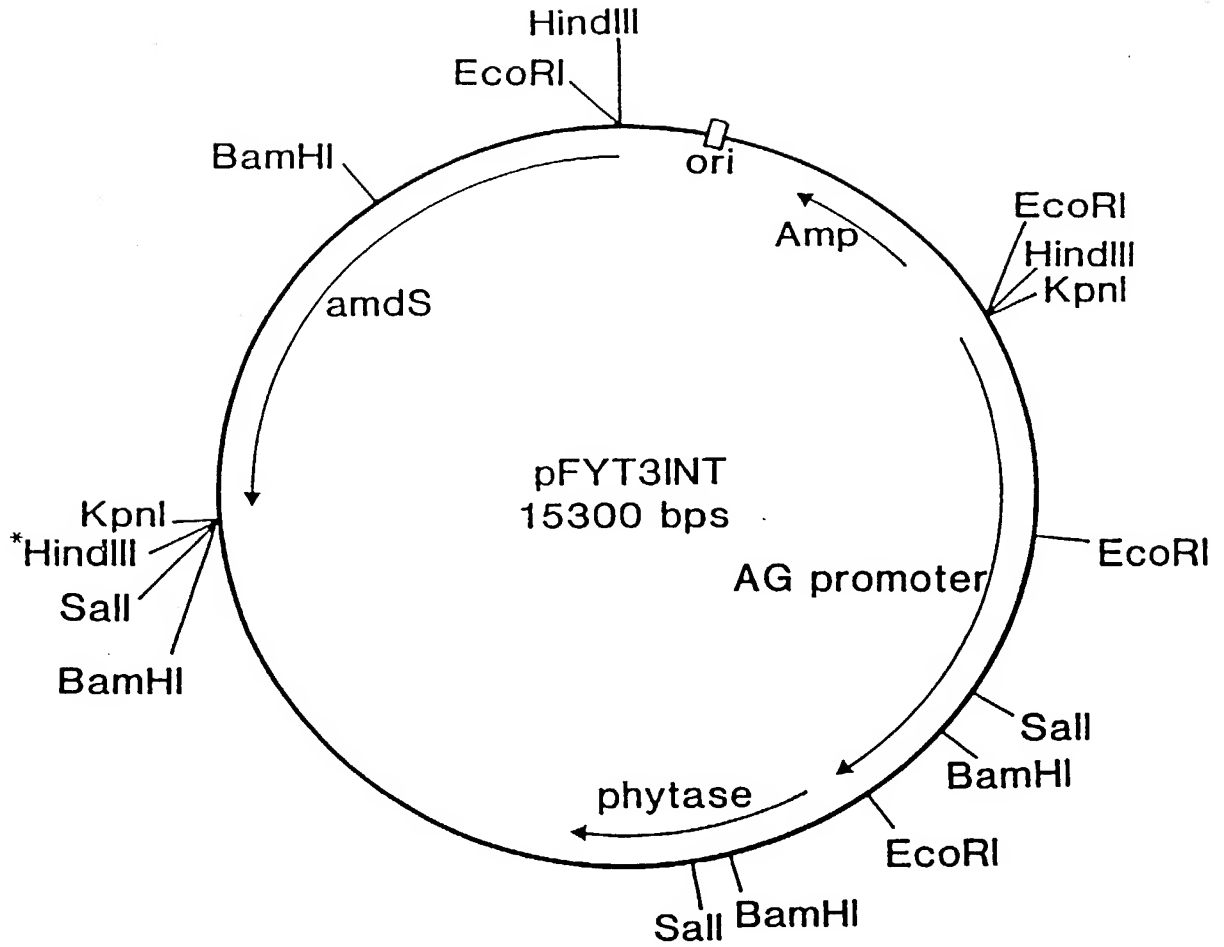


FIG. 17



10079709.110802

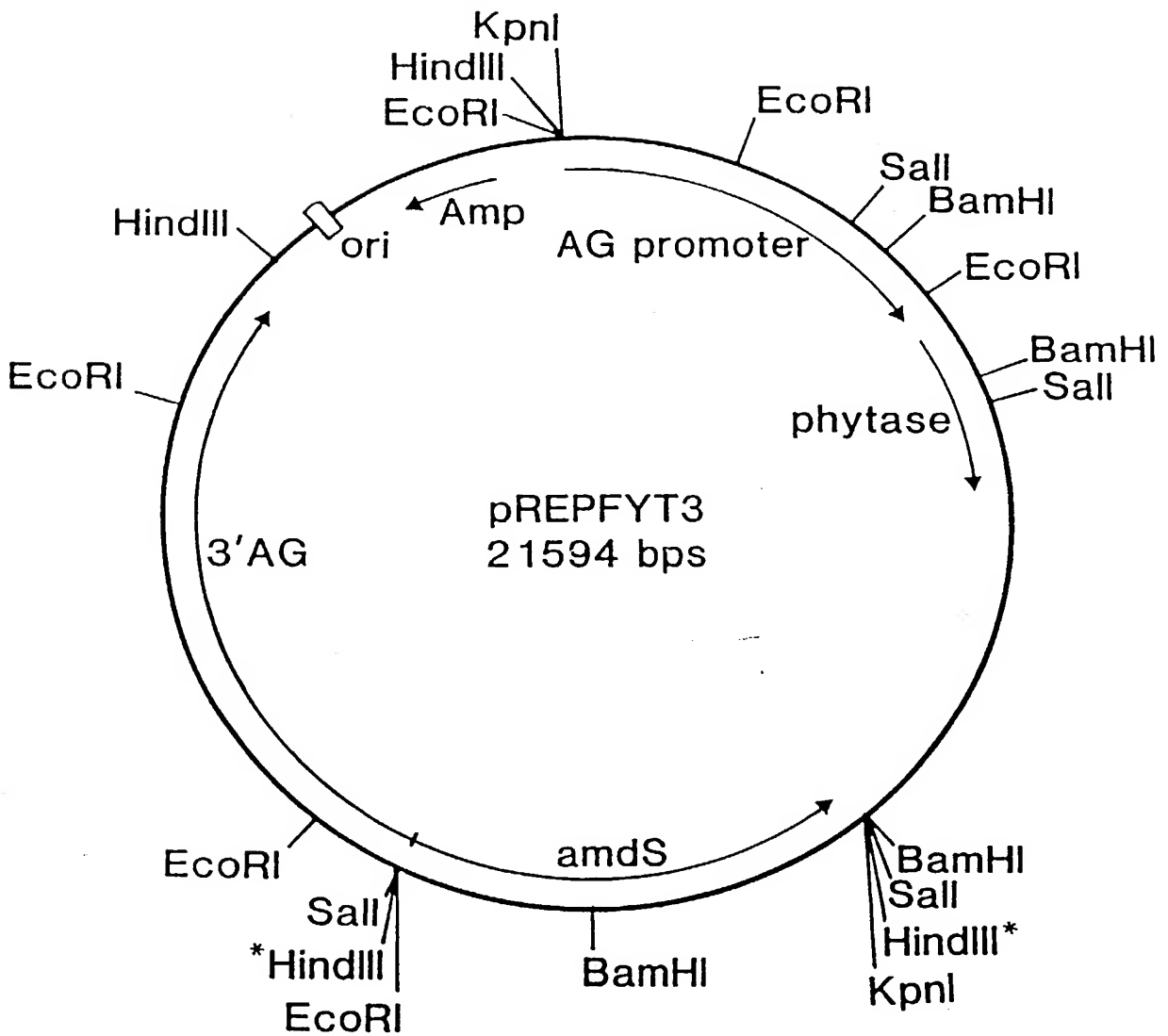


FIG. 18

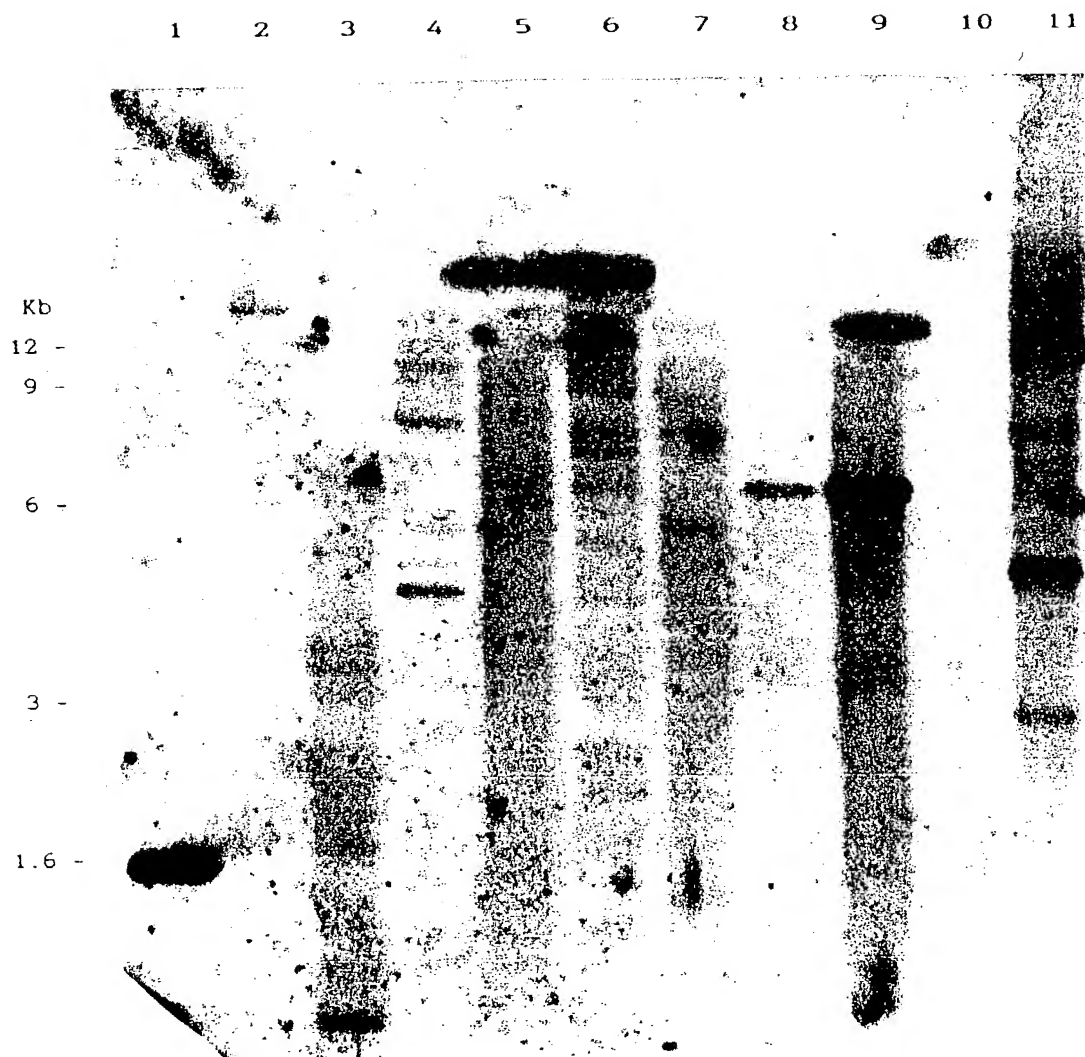


Figure 19A



10079709.110302

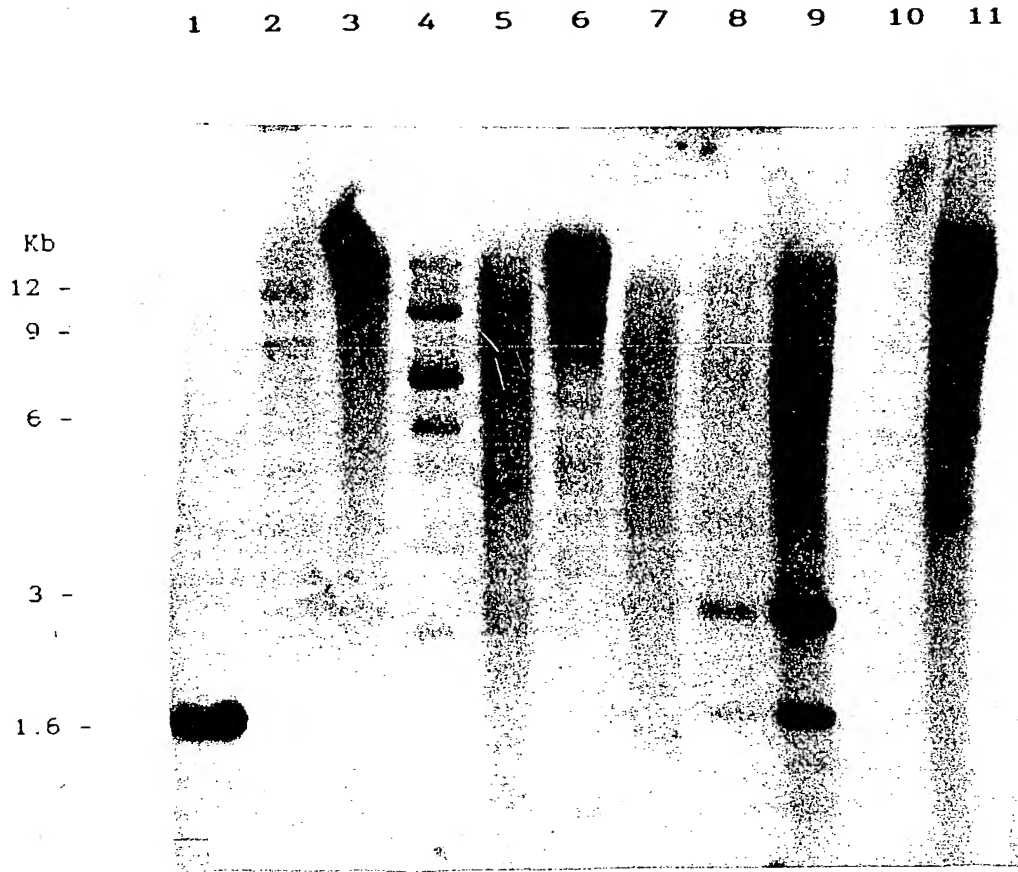


Figure 19B